



Sequence Listing

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Presta, Leonard G.
Shelton, David L.
Urfer, Roman

(ii) TITLE OF INVENTION: Human trk Receptors and Neurotrophic Factor Inhibitors

(iii) NUMBER OF SEQUENCES: 41

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Knobbe, Martens, Olson & Bear
(B) STREET: 620 Newport Center Drive 16th Floor
(C) CITY: Newport Beach
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 92660

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA

(A) APPLICATION NUMBER: 09/724,524
(B) FILING DATE: 27-NOV-2000
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/156,923
(B) FILING DATE: 18-SEP-1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/359,705
(B) FILING DATE: 20-DEC-1994
(C) CLASSIFICATION:

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/286846
(B) FILING DATE: 10-AUG-1994

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/215139
(B) FILING DATE: 18-MAR-1994

(ix) ATTORNEY/AGENT INFORMATION:

(A) NAME: Dreger, Ginger
(B) REGISTRATION NUMBER: 33,055
(C) REFERENCE/DOCKET NUMBER: GENENT.33CP2C2

(x) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: 949/760-0404
 (B) TELEFAX: 949/760-9502
(2) INFORMATION FOR SEQ ID NO:1:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3194 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGAAGGTTTA AAGAAGAAGC CGCAAAGCGC AGGGAAGGCC TCCCGGCACG 50
GGTGGGGGAA AGCGGCCGGT GCAGCGCGGG GACAGGCACT CGGGCTGGCA 100
CTGGCTGCTA GGGATGTCGT CCTGGATAAG GTGGCATGGA CCCGCCATGG 150
CGCGGCTCTG GGGCTTCTGC TGGCTGGTTG TGGGCTTCTG GAGGGCCGCT 200
TTCGCCTGTC CCACGTCCTG CAAATGCAGT GCCTCTCGGA TCTGGTGCAG 250
CGACCCTTCT CCTGGCATCG TGGCATTTCG GAGATTGGAG CCTAACAGTG 300
TAGATCCTGA GAACATCACC GAAATTTTCA TCGCAAACCA GAAAAGGTTA 350
GAAATCATCA ACGAAGATGA TGTGAAGCT TATGTGGGAC TGAGAAATCT 400
GACAATTGTG GATTCTGGAT TAAAATTTGT GGCTCATAAA GCATTTCTGA 450
AAAACAGCAA CCTGCAGCAC ATCAATTTTA CCCGAAACAA ACTGACGAGT 500
TTGTCTAGGA AACATTTCCG TCACCTTGAC TTGTCTGAAC TGATCCTGGT 550
GGGCAATCCA TTTACATGCT CCTGTGACAT TATGTGGATC AAGACTCTCC 600
AAGAGGCTAA ATCCAGTCCA GACACTCAGG ATTTGTACTG CCTGAATGAA 650
AGCAGCAAGA ATATCCCCTT GGCAAACCTG CAGATACCCA ATTGTGGTTT 700
GCCATCTGCA AATCTGGCCG CACCTAACCT CACTGTGGAG GAAGGAAAGT 750
CTATCACATT ATCCTGTAGT GTGGCAGGTG ATCCGGTTCC TAATATGTAT 800
TGGGATGTTG GTAACCTGGT TTCCAAACAT ATGAATGAAA CAAGCCACAC 850
ACAGGGCTCC TTAAGGATAA CTAACATTTT ATCCGATGAC AGTGGGAAGC 900
AGATCTCTTG TGTGGCGGAA AATCTTGTA GAGAAGATCA AGATTCTGTC 950
AACCTCACTG TGCATTTTGC ACCAACTATC ACATTTCTCG AATCTCCAAC 1000
CTCAGACCAC CACTGGTGCA TTCCATTAC TGTGAAAGGC AACCCAAAAC 1050

CAGCGCTTCA GTGGTTCTAT AACGGGGCAA TATTGAATGA GTCCAAATAC 1100
 ATCTGTACTA AAATACATGT TACCAATCAC ACGGAGTACC ACGGCTGCCT 1150
 CCAGCTGGAT AATCCCACCTC ACATGAACAA TGGGGACTAC ACTCTAATAG 1200
 CCAAGAATGA GTATGGGAAG GATGAGAAAC AGATTTCTGC TCACTTCATG 1250
 GGCTGGCCTG GAATTGACGA TGGTGCAAAC CCAAATTATC CTGATGTAAT 1300
 TTATGAAGAT TATGGAAGTG CAGCGAATGA CATCGGGGAC ACCACGAACA 1350
 GAAGTAATGA AATCCCTTCC ACAGACGTCA CTGATAAAAC CGGTCGGGAA 1400
 CATCTCTCGG TCTATGCTGT GGTGGTGATT GCGTCTGTGG TGGGATTTTG 1450
 CCTTTTGGTA ATGCTGTTTC TGCTTAAGTT GGCAAGACAC TCCAAGTTTG 1500
 GCATGAAAGG CCCAGCCTCC GTTATCAGCA ATGATGATGA CTCTGCCAGC 1550
 CCACTCCATC ACATCTCCAA TGGGAGTAAC ACTCCATCTT CTTTCGGAAGG 1600
 TGGCCCAGAT GCTGTCATTA TTGGAATGAC CAAGATCCCT GTCATTGAAA 1650
 ATCCCCAGTA CTTTGGCATC ACCAACAGTC AGCTCAAGCC AGACACATTT 1700
 GTTCAGCACA TCAAGCGACA TAACATTGTT CTGAAAAGGG AGCTAGGCGA 1750
 AGGAGCCTTT GGAAAAGTGT TCCTAGCTGA ATGCTATAAC CTCTGTCCTG 1800
 AGCAGGACAA GATCTTGGTG GCAGTGAAGA CCCTGAAGGA TGCCAGTGAC 1850
 AATGCACGCA AGGACTTCCA CCGTGAGGCC GAGCTCCTGA CCAACCTCCA 1900
 GCATGAGCAC ATCGTCAAGT TCTATGGCGT CTGCGTGGAG GGCGACCCCC 1950
 TCATCATGGT CTTTGAGTAC ATGAAGCATG GGGACCTCAA CAAGTTCCTC 2000
 AGGGCACACG GCCCTGATGC CGTGCTGATG GCTGAGGGCA ACCCGCCCAC 2050
 GGAAGTACG CAGTCGCAGA TGCTGCATAT AGCCCAGCAG ATCGCCGCGG 2100
 GCATGGTCTA CCTGGCGTCC CAGCACTTCG TGCACCGCGA TTTGGCCACC 2150
 AGGAACTGCC TGGTCGGGGA GAACTTGCTG GTGAAAATCG GGGACTTTGG 2200
 GATGTCCCGG GACGTGTACA GCACTGACTA CTACAGGGTC GGTGGCCACA 2250
 CAATGCTGCC CATTCGCTGG ATGCCTCCAG AGAGCATCAT GTACAGGAAA 2300
 TTCACGACGG AAAGCGACGT CTGGAGCCTG GGGGTCGTGT TGTGGGAGAT 2350
 TTTCACCTAT GGCAAACAGC CCTGGTACCA GCTGTCAAAC AATGAGGTGA 2400
 TAGAGTGTAT CACTCAGGGC CGAGTCCTGC AGCGACCCCG CACGTGCCCC 2450
 CAGGAGGTGT ATGAGCTGAT GCTGGGGTGC TGGCAGCGAG AGCCCCACAT 2500

GAGGAAGAAC ATCAAGGGCA TCCATACCCT CCTTCAGAAC TTGGCCAAGG 2550
CATCTCCGGT CTACCTGGAC ATTCTAGGCT AGGGCCCTTT TCCCCAGACC 2600
GATCCTTCCC AACGTACTCC TCAGACGGGC TGAGAGGATG AACATCTTTT 2650
AACTGCCGCT GGAGGCCACC AAGCTGCTCT CCTTCACTCT GACAGTATTA 2700
ACATCAAAGA CTCCGAGAAG CTCTCGAGGG AAGCAGTGTG TACTTCTTCA 2750
TCCATAGACA CAGTATTGAC TTCTTTTTTG CATTATCTCT TTCTCTCTTT 2800
CCATCTCCCT TGGTTGTTCC TTTTCTTTT TTTAAATTTT CTTTTTCTTC 2850
TTTTTTTTCG TCTTCCCTGC TTCACGATTC TTACCCTTTC TTTTGAATCA 2900
ATCTGGCTTC TGCATTACTA TTAAGTCTGC ATAGACAAAG GCCTTAACAA 2950
ACGTAATTTG TTATATCAGC AGACACTCCA GTTTGCCAC CACAACAAAC 3000
AATGCCCTGT TGTATTCCTG CCTTTGATGT GGATGAAAAA AAGGGAAAAC 3050
AAATATTTCA CTTAACTTT GTCACCTCTG CTGTACAGAT ATCGAGAGTT 3100
TCTATGGATT CACTTCTATT TATTTATTAT TATTACTGTT CTTATTGTTT 3150
TTGGATGGCT TAAGCCTGTG TATAAAAAA AAAAAAATC TAGA 3194

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Ser	Trp	Ile	Arg	Trp	His	Gly	Pro	Ala	Met	Ala	Arg	Leu	1	5	10	15
Trp	Gly	Phe	Cys	Trp	Leu	Val	Val	Gly	Phe	Trp	Arg	Ala	Ala	Phe	20	25	30	
Ala	Cys	Pro	Thr	Ser	Cys	Lys	Cys	Ser	Ala	Ser	Arg	Ile	Trp	Cys	35	40	45	
Ser	Asp	Pro	Ser	Pro	Gly	Ile	Val	Ala	Phe	Pro	Arg	Leu	Glu	Pro	50	55	60	
Asn	Ser	Val	Asp	Pro	Glu	Asn	Ile	Thr	Glu	Ile	Phe	Ile	Ala	Asn	65	70	75	
Gln	Lys	Arg	Leu	Glu	Ile	Ile	Asn	Glu	Asp	Asp	Val	Glu	Ala	Tyr	80	85	90	
Val	Gly	Leu	Arg	Asn	Leu	Thr	Ile	Val	Asp	Ser	Gly	Leu	Lys	Phe				

	95	100	105
Val Ala His Lys	Ala Phe Leu Lys Asn Ser Asn Leu Gln His Ile		
	110	115	120
Asn Phe Thr Arg	Asn Lys Leu Thr Ser Leu Ser Arg Lys His Phe		
	125	130	135
Arg His Leu Asp	Leu Ser Glu Leu Ile Leu Val Gly Asn Pro Phe		
	140	145	150
Thr Cys Ser Cys	Asp Ile Met Trp Ile Lys Thr Leu Gln Glu Ala		
	155	160	165
Lys Ser Ser Pro	Asp Thr Gln Asp Leu Tyr Cys Leu Asn Glu Ser		
	170	175	180
Ser Lys Asn Ile	Pro Leu Ala Asn Leu Gln Ile Pro Asn Cys Gly		
	185	190	195
Leu Pro Ser Ala	Asn Leu Ala Ala Pro Asn Leu Thr Val Glu Glu		
	200	205	210
Gly Lys Ser Ile	Thr Leu Ser Cys Ser Val Ala Gly Asp Pro Val		
	215	220	225
Pro Asn Met Tyr	Trp Asp Val Gly Asn Leu Val Ser Lys His Met		
	230	235	240
Asn Glu Thr Ser	His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile		
	245	250	255
Ser Ser Asp Asp	Ser Gly Lys Gln Ile Ser Cys Val Ala Glu Asn		
	260	265	270
Leu Val Gly Glu	Asp Gln Asp Ser Val Asn Leu Thr Val His Phe		
	275	280	285
Ala Pro Thr Ile	Thr Phe Leu Glu Ser Pro Thr Ser Asp His His		
	290	295	300
Trp Cys Ile Pro	Phe Thr Val Lys Gly Asn Pro Lys Pro Ala Leu		
	305	310	315
Gln Trp Phe Tyr	Asn Gly Ala Ile Leu Asn Glu Ser Lys Tyr Ile		
	320	325	330
Cys Thr Lys Ile	His Val Thr Asn His Thr Glu Tyr His Gly Cys		
	335	340	345
Leu Gln Leu Asp	Asn Pro Thr His Met Asn Asn Gly Asp Tyr Thr		
	350	355	360
Leu Ile Ala Lys	Asn Glu Tyr Gly Lys Asp Glu Lys Gln Ile Ser		
	365	370	375
Ala His Phe Met	Gly Trp Pro Gly Ile Asp Asp Gly Ala Asn Pro		

665					670					675				
Asp	Leu	Ala	Thr	Arg	Asn	Cys	Leu	Val	Gly	Glu	Asn	Leu	Leu	Val
				680					685					690
Lys	Ile	Gly	Asp	Phe	Gly	Met	Ser	Arg	Asp	Val	Tyr	Ser	Thr	Asp
				695					700					705
Tyr	Tyr	Arg	Val	Gly	Gly	His	Thr	Met	Leu	Pro	Ile	Arg	Trp	Met
				710					715					720
Pro	Pro	Glu	Ser	Ile	Met	Tyr	Arg	Lys	Phe	Thr	Thr	Glu	Ser	Asp
				725					730					735
Val	Trp	Ser	Leu	Gly	Val	Val	Leu	Trp	Glu	Ile	Phe	Thr	Tyr	Gly
				740					745					750
Lys	Gln	Pro	Trp	Tyr	Gln	Leu	Ser	Asn	Asn	Glu	Val	Ile	Glu	Cys
				755					760					765
Ile	Thr	Gln	Gly	Arg	Val	Leu	Gln	Arg	Pro	Arg	Thr	Cys	Pro	Gln
				770					775					780
Glu	Val	Tyr	Glu	Leu	Met	Leu	Gly	Cys	Trp	Gln	Arg	Glu	Pro	His
				785					790					795
Met	Arg	Lys	Asn	Ile	Lys	Gly	Ile	His	Thr	Leu	Leu	Gln	Asn	Leu
				800					805					810
Ala	Lys	Ala	Ser	Pro	Val	Tyr	Leu	Asp	Ile	Leu	Gly			
				815					820		822			

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1870 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAAGGTTTA AAGAAGAAGC CGCAAAGCGC AGGGAAGGCC TCCCGGCACG 50

GGTGGGGGAA AGCGGCCGGT GCAGCGCGGG GACAGGCACT CGGGCTGGCA 100

CTGGCTGCTA GGGATGTCGT CCTGGATAAG GTGGCATGGA CCCGCCATGG 150

CGCGGCTCTG GGGCTTCTGC TGGCTGGTTG TGGGCTTCTG GAGGGCCGCT 200

TTCGCCTGTC CCACGTCCTG CAAATGCAGT GCCTCTCGGA TCTGGTGACG 250

CGACCCTTCT CCTGGCATCG TGGCATTTCG GAGATTGGAG CCTAACAGTG 300

TAGATCCTGA GAACATCACC GAAATTTTCA TCGCAAACCA GAAAAGGTTA 350

GAATCATCA	ACGAAGATGA	TGTTGAAGCT	TATGTGGGAC	TGAGAAATCT	400
GACAATTGTG	GATTCTGGAT	TAAAATTTGT	GGCTCATAAA	GCATTTCTGA	450
AAAACAGCAA	CCTGCAGCAC	ATCAATTTTA	CCCGAAACAA	ACTGACGAGT	500
TTGTCTAGGA	AACATTTCCG	TCACCTTGAC	TTGTCTGAAC	TGATCCTGGT	550
GGGCAATCCA	TTTACATGCT	CCTGTGACAT	TATGTGGATC	AAGACTCTCC	600
AAGAGGCTAA	ATCCAGTCCA	GACACTCAGG	ATTTGTACTG	CCTGAATGAA	650
AGCAGCAAGA	ATATTCCCCT	GGCAAACCTG	CAGATACCCA	ATTGTGGTTT	700
GCCATCTGCA	AATCTGGCCG	CACCTAACCT	CACTGTGGAG	GAAGGAAAGT	750
CTATCACATT	ATCCTGTAGT	GTGGCAGGTG	ATCCGGTTCC	TAATATGTAT	800
TGGGATGTTG	GTAACCTGGT	TTCCAAACAT	ATGAATGAAA	CAAGCCACAC	850
ACAGGGCTCC	TTAAGGATAA	CTAACATTTT	ATCCGATGAC	AGTGGGAAGC	900
AGATCTCTTG	TGTGGCGGAA	AATCTTGTAG	GAGAAGATCA	AGATTCTGTC	950
AACCTCACTG	TGCATTTTGC	ACCAACTATC	ACATTTCTCG	AATCTCCAAC	1000
CTCAGACCAC	CACTGGTGCA	TTCCATTAC	TGTGAAAGGC	AACCCAAAAC	1050
CAGCGCTTCA	GTGGTTCTAT	AACGGGGCAA	TATTGAATGA	GTCCAAATAC	1100
ATCTGTACTA	AAATACATGT	TACCAATCAC	ACGGAGTACC	ACGGCTGCCT	1150
CCAGCTGGAT	AATCCCCTC	ACATGAACAA	TGGGGACTAC	ACTCTAATAG	1200
CCAAGAATGA	GTATGGGAAG	GATGAGAAAC	AGATTTCTGC	TCACTTCATG	1250
GGCTGGCCTG	GAATTGACGA	TGGTGCAAAC	CCAAATTATC	CTGATGTAAT	1300
TTATGAAGAT	TATGGAAGT	CAGCGAATGA	CATCGGGGAC	ACCACGAACA	1350
GAAGTAATGA	AATCCCCTCC	ACAGACGTCA	CTGATAAAAC	CGGTCGGGAA	1400
CATCTCTCGG	TCTATGCTGT	GGTGGTGATT	GCGTCTGTGG	TGGGATTTTG	1450
CCTTTTGGTA	ATGCTGTTTC	TGCTTAAGTT	GGCAAGACAC	TCCAAGTTTG	1500
GCATGAAAGG	TTTTGTTTTG	TTTCATAAGA	TCCCCTGGA	TGGGTAGCTG	1550
AAATAAAGGA	AAAGACAGAG	AAAGGGGCTG	TGGTGCTTGT	TGGTTGATGC	1600
TGCCATGTAA	GCTGGACTCC	TGGGACTGCT	GTTGGCTTAT	CCCGGGAAGT	1650
GCTGCTTATC	TGGGGTTTTT	TGGTAGATGT	GGGCGGTGTT	TGGAGGCTGT	1700
ACTATATGAA	GCCTGCATAT	ACTGTGAGCT	GTGATTGGGG	AACACCAATG	1750
CAGAGGTAAC	TCTCAGGCAG	CTAAGCAGCA	CCTCAAGAAA	ACATGTTAAA	1800

TTAATGCTTC TCTTCTTACA GTAGTTCAAA TACAAAAC TG AAATGAAATC 1850

CCATTGGATT GTACTTCTCT 1870

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ser	Ser	Trp	Ile	Arg	Trp	His	Gly	Pro	Ala	Met	Ala	Arg	Leu	
1				5					10					15	
Trp	Gly	Phe	Cys	Trp	Leu	Val	Val	Gly	Phe	Trp	Arg	Ala	Ala	Phe	
				20					25					30	
Ala	Cys	Pro	Thr	Ser	Cys	Lys	Cys	Ser	Ala	Ser	Arg	Ile	Trp	Cys	
				35					40					45	
Ser	Asp	Pro	Ser	Pro	Gly	Ile	Val	Ala	Phe	Pro	Arg	Leu	Glu	Pro	
				50					55					60	
Asn	Ser	Val	Asp	Pro	Glu	Asn	Ile	Thr	Glu	Ile	Phe	Ile	Ala	Asn	
				65					70					75	
Gln	Lys	Arg	Leu	Glu	Ile	Ile	Asn	Glu	Asp	Asp	Val	Glu	Ala	Tyr	
				80					85					90	
Val	Gly	Leu	Arg	Asn	Leu	Thr	Ile	Val	Asp	Ser	Gly	Leu	Lys	Phe	
				95					100					105	
Val	Ala	His	Lys	Ala	Phe	Leu	Lys	Asn	Ser	Asn	Leu	Gln	His	Ile	
				110					115					120	
Asn	Phe	Thr	Arg	Asn	Lys	Leu	Thr	Ser	Leu	Ser	Arg	Lys	His	Phe	
				125					130					135	
Arg	His	Leu	Asp	Leu	Ser	Glu	Leu	Ile	Leu	Val	Gly	Asn	Pro	Phe	
				140					145					150	
Thr	Cys	Ser	Cys	Asp	Ile	Met	Trp	Ile	Lys	Thr	Leu	Gln	Glu	Ala	
				155					160					165	
Lys	Ser	Ser	Pro	Asp	Thr	Gln	Asp	Leu	Tyr	Cys	Leu	Asn	Glu	Ser	
				170					175					180	
Ser	Lys	Asn	Ile	Pro	Leu	Ala	Asn	Leu	Gln	Ile	Pro	Asn	Cys	Gly	
				185					190					195	
Leu	Pro	Ser	Ala	Asn	Leu	Ala	Ala	Pro	Asn	Leu	Thr	Val	Glu	Glu	
				200					205					210	
Gly	Lys	Ser	Ile	Thr	Leu	Ser	Cys	Ser	Val	Ala	Gly	Asp	Pro	Val	

215	220	225
Pro Asn Met Tyr Trp Asp Val Gly Asn	Leu Val Ser Lys His Met	
230	235	240
Asn Glu Thr Ser His Thr Gln Gly Ser	Leu Arg Ile Thr Asn Ile	
245	250	255
Ser Ser Asp Asp Ser Gly Lys Gln Ile	Ser Cys Val Ala Glu Asn	
260	265	270
Leu Val Gly Glu Asp Gln Asp Ser Val	Asn Leu Thr Val His Phe	
275	280	285
Ala Pro Thr Ile Thr Phe Leu Glu Ser	Pro Thr Ser Asp His His	
290	295	300
Trp Cys Ile Pro Phe Thr Val Lys Gly	Asn Pro Lys Pro Ala Leu	
305	310	315
Gln Trp Phe Tyr Asn Gly Ala Ile Leu	Asn Glu Ser Lys Tyr Ile	
320	325	330
Cys Thr Lys Ile His Val Thr Asn His	Thr Glu Tyr His Gly Cys	
335	340	345
Leu Gln Leu Asp Asn Pro Thr His Met	Asn Asn Gly Asp Tyr Thr	
350	355	360
Leu Ile Ala Lys Asn Glu Tyr Gly Lys	Asp Glu Lys Gln Ile Ser	
365	370	375
Ala His Phe Met Gly Trp Pro Gly Ile	Asp Asp Gly Ala Asn Pro	
380	385	390
Asn Tyr Pro Asp Val Ile Tyr Glu Asp	Tyr Gly Thr Ala Ala Asn	
395	400	405
Asp Ile Gly Asp Thr Thr Asn Arg Ser	Asn Glu Ile Pro Ser Thr	
410	415	420
Asp Val Thr Asp Lys Thr Gly Arg Glu	His Leu Ser Val Tyr Ala	
425	430	435
Val Val Val Ile Ala Ser Val Val Gly	Phe Cys Leu Leu Val Met	
440	445	450
Leu Phe Leu Leu Lys Leu Ala Arg His	Ser Lys Phe Gly Met Lys	
455	460	465
Gly Phe Val Leu Phe His Lys Ile Pro	Leu Asp Gly	
470	475	477

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2715 base pairs

(B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGATCCGCGT CGGAGATGGA TGTCTCTCTT TGCCAGCCA AGTGTAGTTT 50
 CTGGCGGATT TTCTTGCTGG GAAGCGTCTG GCTGGACTAT GTGGGCTCCG 100
 TGCTGGCTTG CCCTGCAAAT TGTGTCTGCA GCAAGACTGA GATCAATTGC 150
 CGGCGGCCGG ACGATGGGAA CCTCTTCCCC CTCCTGGAAG GGCAGGATTC 200
 AGGGAACAGC AATGGGAACG CCAATATCAA CATCACGGAC ATCTCAAGGA 250
 ATATCACTTC CATAACATA GAGAACTGGC GCAGTCTTCA CACGCTCAAC 300
 GCCGTGGACA TGGAGCTCTA CACCGGACTT CAAAAGCTGA CCATCAAGAA 350
 CTCAGGACTT CGGAGCATTC AGCCAGAGC CTTTGCCAAG AACCCCCATT 400
 TGCGTTATAT AAACCTGTCA AGTAACCGGC TCACCACACT CTCGTGGCAG 450
 CTCTTCCAGA CGCTGAGTCT TCGGGAATTG CAGTTGGAGC AGAACTTTTT 500
 CAACTGCAGC TGTGACATCC GCTGGATGCA GCTCTGGCAG GAGCAGGGGG 550
 AGGCCAAGCT CAACAGCCAG AACCTCTACT GCATCAATGC TGATGGCTCC 600
 CAGCTTCCTC TCTTCCGCAT GAACATCAGT CAGTGTGACC TTCCTGAGAT 650
 CAGCGTGAGC CACGTCAACC TGACCGTACG AGAGGGTGAC AATGCTGTTA 700
 TCACTTGCAA TGGCTCTGGA TCACCCCTTC CTGATGTGGA CTGGATAGTC 750
 ACTGGGCTGC AGTCCATCAA CACTCACCAG ACCAATCTGA ACTGGACCAA 800
 TGTTTCATGCC ATCAACTTGA CGCTGGTGAA TGTGACGAGT GAGGACAATG 850
 GCTTCACCCT GACGTGCATT GCAGAGAACG TGGTGGGCAT GAGCAATGCC 900
 AGTGTGCCC TCACTGTCTA CTATCCCCCA CGTGTGGTGA GCCTGGAGGA 950
 GCCTGAGCTG CGCCTGGAGC ACTGCATCGA GTTTGTGGTG CGTGGCAACC 1000
 CCCACCAAC GCTGCACTGG CTGCACAATG GGCAGCCTCT GCGGGAGTCC 1050
 AAGATCATCC ATGTGGAATA CTACCAAGAG GGAGAGATTT CCGAGGGCTG 1100
 CCTGCTCTTC AACAAAGCCCA CCCACTACAA CAATGGCAAC TATACCCTCA 1150
 TTGCCAAAAA CCCACTGGGC ACAGCCAACC AGACCATCAA TGGCCACTTC 1200
 CTCAAGGAGC CCTTTCCAGA GAGCACGGAT AACTTTATCT TGTTTGACGA 1250

AGTGAGTCCC ACACCTCCTA TCACTGTGAC CCACAAACCA GAAGAAGACA 1300
 CTTTTGGGGT ATCCATAGCA GTTGGACTTG CTGCTTTTGC CTGTGTCCTG 1350
 TTGGTGGTTC TCTTCGTCAT GATCAACAAA TATGGTCGAC GGTCCAAATT 1400
 TGGAATGAAG GGTCCCGTGG CTGTCATCAG TGGTGAGGAG GACTCAGCCA 1450
 GCCCACTGCA CCACATCAAC CACGGCATCA CCACGCCCTC GTCCTGGAT 1500
 GCCGGGCCCCG AACTGTGGT CATTGGCATG ACTCGCATCC CTGTCATTGA 1550
 GAACCCCCAG TACTTCCGTC AGGGACACAA CTGCCACAAG CCGGACACGT 1600
 ATGTGCAGCA CATTAAGAGG AGAGACATCG TGCTGAAGCG AGAACTGGGT 1650
 GAGGGAGCCT TTGGAAAGGT CTTCTGGGCC GAGTGCTACA ACCTCAGCCC 1700
 GACCAAGGAC AAGATGCTTG TGGCTGTGAA GGCCCTGAAG GATCCCACCC 1750
 TGGCTGCCCCG GAAGGATTTT CAGAGGGAGG CCGAGCTGCT CACCAACCTG 1800
 CAGCATGAGC ACATTGTCAA GTTCTATGGA GTGTGCGGCG ATGGGGACCC 1850
 CCTCATCATG GTCTTTGAAT ACATGAAGCA TGGAGACCTG AATAAGTTCC 1900
 TCAGGGCCCA TGGGCCAGAT GCAATGATCC TTGTGGATGG ACAGCCACGC 1950
 CAGGCCAAGG GTGAGCTGGG GCTCTCCCAA ATGCTCCACA TTGCCAGTCA 2000
 GATCGCCTCG GGTATGGTGT ACCTGGCCTC CCAGCACTTT GTGCACCGAG 2050
 ACCTGGCCAC CAGGAACTGC CTGGTTGGAG CGAATCTGCT AGTGAAGATT 2100
 GGGGACTTCG GCATGTCCAG AGATGTCTAC AGCACGGATT ATTACAGGCT 2150
 CTTTAATCCA TCTGGAAATG ATTTTTGTAT ATGGTGTGAG GTGGGAGGAC 2200
 ACACCATGCT CCCCATTCGC TGGATGCCTC CTGAAAGCAT CATGTACCGG 2250
 AAGTTCAC TA CAGAGAGTGA TGTATGGAGC TTCGGGGTGA TCCTCTGGGA 2300
 GATCTTCACC TATGGAAAGC AGCCATGGTT CCAACTCTCA AACACGGAGG 2350
 TCATTGAGTG CATTACCCAA GGTCGTGTTT TGGAGCGGCC CCGAGTCTGC 2400
 CCCAAAGAGG TGTACGATGT CATGCTGGGG TGCTGGCAGA GGGAACCACA 2450
 GCAGCGGTTG AACATCAAGG AGATCTACAA AATCCTCCAT GCTTTGGGGA 2500
 AGGCCACCCC AATCTACCTG GACATTCTTG GCTAGTGGTG GCTGGTGGTC 2550
 ATGAATTCAT ACTCTGTTGC CTCCTCTCTC CCTGCCTCAC ATCTCCCTTC 2600
 CACCTCACAA CTCCTTCCAT CCTTGACTGA AGCGAACATC TTCATATAAA 2650
 CTCAAGTGCC TGCTACACAT ACAACACTGA AAAAAGGAAA AAAAAAGAAA 2700

AAAAAAAAAA ACCGC 2715

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 839 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asp	Val	Ser	Leu	Cys	Pro	Ala	Lys	Cys	Ser	Phe	Trp	Arg	Ile	1	5	10	15
Phe	Leu	Leu	Gly	Ser	Val	Trp	Leu	Asp	Tyr	Val	Gly	Ser	Val	Leu	20	25	30	
Ala	Cys	Pro	Ala	Asn	Cys	Val	Cys	Ser	Lys	Thr	Glu	Ile	Asn	Cys	35	40	45	
Arg	Arg	Pro	Asp	Asp	Gly	Asn	Leu	Phe	Pro	Leu	Leu	Glu	Gly	Gln	50	55	60	
Asp	Ser	Gly	Asn	Ser	Asn	Gly	Asn	Ala	Asn	Ile	Asn	Ile	Thr	Asp	65	70	75	
Ile	Ser	Arg	Asn	Ile	Thr	Ser	Ile	His	Ile	Glu	Asn	Trp	Arg	Ser	80	85	90	
Leu	His	Thr	Leu	Asn	Ala	Val	Asp	Met	Glu	Leu	Tyr	Thr	Gly	Leu	95	100	105	
Gln	Lys	Leu	Thr	Ile	Lys	Asn	Ser	Gly	Leu	Arg	Ser	Ile	Gln	Pro	110	115	120	
Arg	Ala	Phe	Ala	Lys	Asn	Pro	His	Leu	Arg	Tyr	Ile	Asn	Leu	Ser	125	130	135	
Ser	Asn	Arg	Leu	Thr	Thr	Leu	Ser	Trp	Gln	Leu	Phe	Gln	Thr	Leu	140	145	150	
Ser	Leu	Arg	Glu	Leu	Gln	Leu	Glu	Gln	Asn	Phe	Phe	Asn	Cys	Ser	155	160	165	
Cys	Asp	Ile	Arg	Trp	Met	Gln	Leu	Trp	Gln	Glu	Gln	Gly	Glu	Ala	170	175	180	
Lys	Leu	Asn	Ser	Gln	Asn	Leu	Tyr	Cys	Ile	Asn	Ala	Asp	Gly	Ser	185	190	195	
Gln	Leu	Pro	Leu	Phe	Arg	Met	Asn	Ile	Ser	Gln	Cys	Asp	Leu	Pro	200	205	210	
Glu	Ile	Ser	Val	Ser	His	Val	Asn	Leu	Thr	Val	Arg	Glu	Gly	Asp	215	220	225	

Pro Lys Glu Val Tyr Asp Val Met Leu Gly Cys Trp Gln Arg Glu
800 805 810

Pro Gln Gln Arg Leu Asn Ile Lys Glu Ile Tyr Lys Ile Leu His
815 820 825

Ala Leu Gly Lys Ala Thr Pro Ile Tyr Leu Asp Ile Leu Gly
830 835 839

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1858 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGATCCGCGT CGGAGATGGA TGTCTCTCTT TGCCCAGCCA AGTGTAGTTT 50
CTGGCGGATT TTCTTGCTGG GAAGCGTCTG GCTGGACTAT GTGGGCTCCG 100
TGCTGGCTTG CCCTGCAAAT TGTGTCTGCA GCAAGACTGA GATCAATTGC 150
CGGCGGCCGG ACGATGGGAA CCTCTTCCCC CTCCTGGAAG GGCAGGATTC 200
AGGGAACAGC AATGGGAACG CCAATATCAA CATCACGGAC ATCTCAAGGA 250
ATATCACTTC CATAACATA GAGAACTGGC GCAGTCTTCA CACGCTCAAC 300
GCCGTGGACA TGGAGCTCTA CACCGGACTT CAAAAGCTGA CCATCAAGAA 350
CTCAGGACTT CGGAGCATTC AGCCCAGAGC CTTTGCCAAG AACCCCCATT 400
TGCGTTATAT AAACCTGTCA AGTAACCGGC TCACCACACT CTCGTGGCAG 450
CTCTTCCAGA CGCTGAGTCT TCGGGAATTG CAGTTGGAGC AGAACTTTTT 500
CAACTGCAGC TGTGACATCC GCTGGATGCA GCTCTGGCAG GAGCAGGGGG 550
AGGCCAAGCT CAACAGCCAG AACCTCTACT GCATCAATGC TGATGGCTCC 600
CAGCTTCCTC TCTTCCGCAT GAACATCAGT CAGTGTGACC TTCCTGAGAT 650
CAGCGTGAGC CACGTCAACC TGACCGTACG AGAGGGTGAC AATGCTGTTA 700
TCACTTGCAA TGGCTCTGGA TCACCCCTTC CTGATGTGGA CTGGATAGTC 750
ACTGGGCTGC AGTCCATCAA CACTCACCAG ACCAATCTGA ACTGGACCAA 800
TGTTCATGCC ATCAACTTGA CGCTGGTGAA TGTGACGAGT GAGGACAATG 850
GCTTACCCT GACGTGCATT GCAGAGAACG TGGTGGGCAT GAGCAATGCC 900
AGTGTTGCCC TCACTGTCTA CTATCCCCCA CGTGTGGTGA GCCTGGAGGA 950

GCCTGAGCTG CGCCTGGAGC ACTGCATCGA GTTTGTGGTG CGTGGCAACC 1000
 CCCCACCAAC GCTGCACTGG CTGCACAATG GGCAGCCTCT GCGGGAGTCC 1050
 AAGATCATCC ATGTGGAATA CTACCAAGAG GGAGAGATTT CCGAGGGCTG 1100
 CCTGCTCTTC AACAAAGCCCA CCCACTACAA CAATGGCAAC TATACCCTCA 1150
 TTGCCAAAAA CCCACTGGGC ACAGCCAACC AGACCATCAA TGGCCACTTC 1200
 CTCAAGGAGC CCTTTCCAGA GAGCACGGAT AACTTTATCT TGTTTGACGA 1250
 AGTGAGTCCC ACACCTCCTA TCACTGTGAC CCACAAACCA GAAGAAGACA 1300
 CTTTTGGGGT ATCCATAGCA GTTGGACTTG CTGCTTTTGC CTGTGTCCTG 1350
 TTGGTGGTTC TCTTCGTCAT GATCAACAAA TATGGTCGAC GGTCCAAATT 1400
 TGGAATGAAG GGTCCTGTGG CTGTCATCAG TGGTGAGGAG GACTCAGCCA 1450
 GCCCACTGCA CCACATCAAC CACGGCATCA CCACGCCCTC GTCACTGGAT 1500
 GCCGGGCCCCG ACACTGTGGT CATTGGCATG ACTCGCATCC CTGTCATTGA 1550
 GAACCCCCAG TACTTCCGTC AGGGACACAA CTGCCACAAG CCGGACACGT 1600
 GGGTCTTTTC AAACATAGAC AATCATGGGA TATTAACTT GAAGGACAAT 1650
 AGAGATCATC TAGTCCCATC AACTCACTAT ATATATGAGG AACCTGAGGT 1700
 CCAGAGTGGG GAAGTGTCTT ACCCAAGGTC ACATGGTTTC AGAGAAATTA 1750
 TGTTGAATCC AATAAGCCTT CCCGGACATT CCAAGCCTCT TAACCATGGC 1800
 ATCTATGTTG AGGATGTCAA TGTTTATTTT AGCAAAGGAC GTCATGGCCT 1850
 TTAAAAAC 1858

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 612 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Asp	Val	Ser	Leu	Cys	Pro	Ala	Lys	Cys	Ser	Phe	Trp	Arg	Ile
1				5				10						15
Phe	Leu	Leu	Gly	Ser	Val	Trp	Leu	Asp	Tyr	Val	Gly	Ser	Val	Leu
			20					25						30
Ala	Cys	Pro	Ala	Asn	Cys	Val	Cys	Ser	Lys	Thr	Glu	Ile	Asn	Cys
			35					40						45

Pro	Thr	Leu	His	Trp	Leu	His	Asn	Gly	Gln	Pro	Leu	Arg	Glu	Ser	335	340	345
Lys	Ile	Ile	His	Val	Glu	Tyr	Tyr	Gln	Glu	Gly	Glu	Ile	Ser	Glu	350	355	360
Gly	Cys	Leu	Leu	Phe	Asn	Lys	Pro	Thr	His	Tyr	Asn	Asn	Gly	Asn	365	370	375
Tyr	Thr	Leu	Ile	Ala	Lys	Asn	Pro	Leu	Gly	Thr	Ala	Asn	Gln	Thr	380	385	390
Ile	Asn	Gly	His	Phe	Leu	Lys	Glu	Pro	Phe	Pro	Glu	Ser	Thr	Asp	395	400	405
Asn	Phe	Ile	Leu	Phe	Asp	Glu	Val	Ser	Pro	Thr	Pro	Pro	Ile	Thr	410	415	420
Val	Thr	His	Lys	Pro	Glu	Glu	Asp	Thr	Phe	Gly	Val	Ser	Ile	Ala	425	430	435
Val	Gly	Leu	Ala	Ala	Phe	Ala	Cys	Val	Leu	Leu	Val	Val	Leu	Phe	440	445	450
Val	Met	Ile	Asn	Lys	Tyr	Gly	Arg	Arg	Ser	Lys	Phe	Gly	Met	Lys	455	460	465
Gly	Pro	Val	Ala	Val	Ile	Ser	Gly	Glu	Glu	Asp	Ser	Ala	Ser	Pro	470	475	480
Leu	His	His	Ile	Asn	His	Gly	Ile	Thr	Thr	Pro	Ser	Ser	Leu	Asp	485	490	495
Ala	Gly	Pro	Asp	Thr	Val	Val	Ile	Gly	Met	Thr	Arg	Ile	Pro	Val	500	505	510
Ile	Glu	Asn	Pro	Gln	Tyr	Phe	Arg	Gln	Gly	His	Asn	Cys	His	Lys	515	520	525
Pro	Asp	Thr	Trp	Val	Phe	Ser	Asn	Ile	Asp	Asn	His	Gly	Ile	Leu	530	535	540
Asn	Leu	Lys	Asp	Asn	Arg	Asp	His	Leu	Val	Pro	Ser	Thr	His	Tyr	545	550	555
Ile	Tyr	Glu	Glu	Pro	Glu	Val	Gln	Ser	Gly	Glu	Val	Ser	Tyr	Pro	560	565	570
Arg	Ser	His	Gly	Phe	Arg	Glu	Ile	Met	Leu	Asn	Pro	Ile	Ser	Leu	575	580	585
Pro	Gly	His	Ser	Lys	Pro	Leu	Asn	His	Gly	Ile	Tyr	Val	Glu	Asp	590	595	600
Val	Asn	Val	Tyr	Phe	Ser	Lys	Gly	Arg	His	Gly	Phe				605	610	612

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 790 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Leu	Arg	Gly	Gly	Arg	Arg	Gly	Gln	Leu	Gly	Trp	His	Ser	Trp	1	5	10	15
Ala	Ala	Gly	Pro	Gly	Ser	Leu	Leu	Ala	Trp	Leu	Ile	Leu	Ala	Ser	20	25	30	
Ala	Gly	Ala	Ala	Pro	Cys	Pro	Asp	Ala	Cys	Cys	Pro	His	Gly	Ser	35	40	45	
Ser	Gly	Leu	Arg	Cys	Thr	Arg	Asp	Gly	Ala	Leu	Asp	Ser	Leu	His	50	55	60	
His	Leu	Pro	Gly	Ala	Glu	Asn	Leu	Thr	Glu	Leu	Tyr	Ile	Glu	Asn	65	70	75	
Gln	Gln	His	Leu	Gln	His	Leu	Glu	Leu	Arg	Asp	Leu	Arg	Gly	Leu	80	85	90	
Gly	Glu	Leu	Arg	Asn	Leu	Thr	Ile	Val	Lys	Ser	Gly	Leu	Arg	Phe	95	100	105	
Val	Ala	Pro	Asp	Ala	Phe	His	Phe	Thr	Pro	Arg	Leu	Ser	Arg	Leu	110	115	120	
Asn	Leu	Ser	Phe	Asn	Ala	Leu	Glu	Ser	Leu	Ser	Trp	Lys	Thr	Val	125	130	135	
Gln	Gly	Leu	Ser	Leu	Gln	Glu	Leu	Val	Leu	Ser	Gly	Asn	Pro	Leu	140	145	150	
His	Cys	Ser	Cys	Ala	Leu	Arg	Trp	Leu	Gln	Arg	Trp	Glu	Glu	Glu	155	160	165	
Gly	Leu	Gly	Gly	Val	Pro	Glu	Gln	Lys	Leu	Gln	Cys	His	Gly	Gln	170	175	180	
Gly	Pro	Leu	Ala	His	Met	Pro	Asn	Ala	Ser	Cys	Gly	Val	Pro	Thr	185	190	195	
Leu	Lys	Val	Gln	Val	Pro	Asn	Ala	Ser	Val	Asp	Val	Gly	Asp	Asp	200	205	210	
Val	Leu	Leu	Arg	Cys	Gln	Val	Glu	Gly	Arg	Gly	Leu	Glu	Gln	Ala	215	220	225	
Gly	Trp	Ile	Leu	Thr	Glu	Leu	Glu	Gln	Ser	Ala	Thr	Val	Met	Lys	230	235	240	

Leu	Leu	Pro	Glu	Gln	Asp	Lys	Met	Leu	Val	Ala	Val	Lys	Ala	Leu	530	535	540
Lys	Glu	Ala	Ser	Glu	Ser	Ala	Arg	Gln	Asp	Phe	Gln	Arg	Glu	Ala	545	550	555
Glu	Leu	Leu	Thr	Met	Leu	Gln	His	Gln	His	Ile	Val	Arg	Phe	Phe	560	565	570
Gly	Val	Cys	Thr	Glu	Gly	Arg	Pro	Leu	Leu	Met	Val	Phe	Glu	Tyr	575	580	585
Met	Arg	His	Gly	Asp	Leu	Asn	Arg	Phe	Leu	Arg	Ser	His	Gly	Pro	590	595	600
Asp	Ala	Lys	Leu	Leu	Ala	Gly	Gly	Glu	Asp	Val	Ala	Pro	Gly	Pro	605	610	615
Leu	Gly	Leu	Gly	Gln	Leu	Leu	Ala	Val	Ala	Ser	Gln	Val	Ala	Ala	620	625	630
Gly	Met	Val	Tyr	Leu	Ala	Gly	Leu	His	Phe	Val	His	Arg	Asp	Leu	635	640	645
Ala	Thr	Arg	Asn	Cys	Leu	Val	Gly	Gln	Gly	Leu	Val	Val	Lys	Ile	650	655	660
Gly	Asp	Phe	Gly	Met	Ser	Arg	Asp	Ile	Tyr	Ser	Thr	Asp	Tyr	Tyr	665	670	675
Arg	Val	Gly	Gly	Arg	Thr	Met	Leu	Pro	Ile	Arg	Trp	Met	Pro	Pro	680	685	690
Glu	Ser	Ile	Leu	Tyr	Arg	Lys	Phe	Thr	Thr	Glu	Ser	Asp	Val	Trp	695	700	705
Ser	Phe	Gly	Val	Val	Leu	Trp	Glu	Ile	Phe	Thr	Tyr	Gly	Lys	Gln	710	715	720
Pro	Trp	Tyr	Gln	Leu	Ser	Asn	Thr	Glu	Ala	Ile	Asp	Cys	Ile	Thr	725	730	735
Gln	Gly	Arg	Glu	Leu	Glu	Arg	Pro	Arg	Ala	Cys	Pro	Pro	Glu	Val	740	745	750
Tyr	Ala	Ile	Met	Arg	Gly	Cys	Trp	Gln	Arg	Glu	Pro	Gln	Gln	Arg	755	760	765
His	Ser	Ile	Lys	Asp	Val	His	Ala	Arg	Leu	Gln	Ala	Leu	Ala	Gln	770	775	780
Ala	Pro	Pro	Val	Tyr	Leu	Asp	Val	Leu	Gly						785	790	

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGYGAYATHA TGTGGYTNAAC RAC 23

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGGATGCARY TNTGGCARCA RCA 23

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

YTCRTCYYTN CCRTAYTCRT T 21

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCYTCYTGRAT ARTAYTCNAC GTG 23

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CACGTCAACA ACGGCAACTA CA 22

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGAAGGATGA GAAACAGATT TCTGC 25

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CATCAATGGC CACTTCCTCA AGG 23

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGGTGTTTCG TCCTTCTTCT CC 22

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAGATGTGCC CGACCGGTTG TATC 24

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CACAGTGATA GGAGGTGTGG GA 22

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGATGTGGCT CCAGGCCCC 19

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGGCAACCCG CCCACGGAA 19

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACGCCAGGCC AAGGGTGAG 19

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: Nucleic Acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TAACCACTCC CAGCCCCTGG 20

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTGGTGGCCT CCAGCGGCAG 20

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AATTCATGAC CACCAGCCAC CA 22

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCTCCTCGGG ACTGCGATGC 20

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGTCGCCCT GGCCGAGGTG GCAT 24

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAGCTCAACA GCCAGAACCT C 21

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAGCTCTGTG AGGATCCAGC C 21

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCGACCGGTT TTATCAGTGA C 21

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGATCTTGG ACTCCCGCAG AGG 23

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTTGGCCAAG GCATCTCCGG T 21

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGTGCAGCA CATTAAGAGG A 21

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TTATACACAG GCTTAAGCCA TCCA 24

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGGAGGCATC CAGCGAATG 19

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

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(2) INFORMATION FOR SEQ ID NO:37:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

(2) INFORMATION FOR SEQ ID NO:38:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

(2) INFORMATION FOR SEQ ID NO:39:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

(2) INFORMATION FOR SEQ ID NO:40:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

(2) INFORMATION FOR SEQ ID NO:41:

29

(A) LENGTH: 84 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Trp	Val	Phe	Ser	Asn	Ile	Asp	Asn	His	Gly	Ile	Leu	Asn	Leu	Lys
1				5					10					15
Asp	Asn	Arg	Asp	His	Leu	Val	Pro	Ser	Thr	His	Tyr	Ile	Tyr	Glu
				20					25					30
Glu	Pro	Glu	Val	Gln	Ser	Gly	Glu	Val	Ser	Tyr	Pro	Arg	Ser	His
				35					40					45
Gly	Phe	Arg	Glu	Ile	Met	Leu	Asn	Pro	Ile	Ser	Leu	Pro	Gly	His
				50					55					60
Ser	Lys	Pro	Leu	Asn	His	Gly	Ile	Tyr	Val	Glu	Asp	Val	Asn	Val
				65					70					75
Tyr	Phe	Ser	Lys	Gly	Arg	His	Gly	Phe						
				80				84						

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